

RAW SEQUENCE LISTING

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Application Serial Number: 10/569,022
Source: IFWP
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IFWP

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DATE: 03/07/2006

PATENT APPLICATION: US/10/569,022

TIME: 10:10:39

Input Set : E:\Final Sequence list-13173-00025-US.txt

Output Set: N:\CRF4\03072006\J569022.raw

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3 <110> APPLICANT: Flachmann, Ralf
4     Schopfer, Christel Renate
5     Herbers, Karin
6     Kunze, Irene
7     Sauer, Matt
8     Klebsattel, Martin
9     Luck, Thomas
10    Voeste, Dirk
11    Pfeiffer, Angelika-Maria
13 <120> TITLE OF INVENTION: Method for producing ketocarotenoids in genetically
modified,
14    non-human organisms
16 <130> FILE REFERENCE: 13173-00025-US
C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/569,022
C--> 18 <141> CURRENT FILING DATE: 2006-02-17
18 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/008623
19 <151> PRIOR FILING DATE: 2004-07-31
21 <150> PRIOR APPLICATION NUMBER: PCT/EP03/09102
22 <151> PRIOR FILING DATE: 2003-08-18
24 <150> PRIOR APPLICATION NUMBER: PCT/EP03/09107
25 <151> PRIOR FILING DATE: 2003-08-18
27 <150> PRIOR APPLICATION NUMBER: PCT/EP03/09105
28 <151> PRIOR FILING DATE: 2003-08-18
30 <150> PRIOR APPLICATION NUMBER: PCT/EP03/09106
31 <151> PRIOR FILING DATE: 2003-08-18
33 <150> PRIOR APPLICATION NUMBER: PCT/EP03/09109
34 <151> PRIOR FILING DATE: 2003-08-18
36 <150> PRIOR APPLICATION NUMBER: PCT/EP03/09101
37 <151> PRIOR FILING DATE: 2003-08-18
39 <150> PRIOR APPLICATION NUMBER: DE 102004007622.7
40 <151> PRIOR FILING DATE: 2004-02-17
42 <160> NUMBER OF SEQ ID NOS: 137
44 <170> SOFTWARE: PatentIn version 3.3
48 <210> SEQ ID NO: 1
49 <211> LENGTH: 1666
50 <212> TYPE: DNA
51 <213> ORGANISM: Lycopersicon esculentum
53 <220> FEATURE:
54 <221> NAME/KEY: CDS
55 <222> LOCATION: (1)..(1494)
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60 Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Leu Ser Ser Pro
61 1                               5                               10                               15

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63	aca ccc cat agg tct att ttc caa caa aat ccc tct ttt cta agt ccc	96
64	Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro	
65	20 25 30	
67	acc acc aaa aaa aaa tca aga aaa tgt ctt ctt aga aac aaa agt agt	144
68	Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser	
69	35 40 45	
71	aaa ctt ttt tgt agc ttt ctt gat tta gca ccc aca tca aag cca gag	192
72	Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu	
73	50 55 60	
75	tct tta gat gtt aac atc tca tgg gtt gat cct aat tgc aat cgg gct	240
76	Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala	
77	65 70 75 80	
79	caa ttc gac gtg atc att atc gga gct ggc cct gct ggg ctc agg cta	288
80	Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu	
81	85 90 95	
83	gct gaa caa gtt tct aaa tat ggt att aag gta tgt tgt gtt gac cct	336
84	Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro	
85	100 105 110	
87	tca cca ctc tcc atg tgg cca aat aat tat ggt gtt tgg gtt gat gag	384
88	Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu	
89	115 120 125	
91	ttt gag aat tta gga ctg gaa aat tgt tta gat cat aaa tgg cct atg	432
92	Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met	
93	130 135 140	
95	act tgt gtg cat ata aat gat aac aaa act aag tat ttg gga aga cca	480
96	Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro	
97	145 150 155 160	
99	tat ggt aga gtt agt aga aag aag ctg aag ttg aaa ttg ttg aat agt	528
100	Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Asn Ser	
101	165 170 175	
103	tgt gtt gag aac aga gtg aag ttt tat aaa gct aag gtt tgg aaa gtg	576
104	Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val	
105	180 185 190	
107	gaa cat gaa gaa ttt gag tct tca att gtt tgt gat gat ggt aag aag	624
108	Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys	
109	195 200 205	
111	ata aga ggt agt ttg gtt gtg gat gca agt ggt ttt gct agt gat ttt	672
112	Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe	
113	210 215 220	
115	ata gag tat gac agg cca aga aac cat ggt tat caa att gct cat ggg	720
116	Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly	
117	225 230 235 240	
119	ggt tta gta gaa gtt gat aat cat cca ttt gat ttg gat aaa atg gtg	768
120	Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val	
121	245 250 255	
123	ctt atg gat tgg agg gat tct cat ttg ggt aat gag cca tat tta agg	816
124	Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg	
125	260 265 270	
127	gtg aat aat gct aaa gaa cca aca ttc ttg tat gca atg cca ttt gat	864

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128 Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp
129          275                      280                      285
131 aga gat ttg gtt ttc ttg gaa gag act tct ttg gtg agt cgt cct gtt      912
132 Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val
133          290                      295                      300
135 tta tcg tat atg gaa gta aaa aga agg atg gtg gca aga tta agg cat      960
136 Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His
137 305                      310                      315                      320
139 ttg ggg atc aaa gtg aaa agt gtt att gag gaa gag aaa tgt gtg atc      1008
140 Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Glu Lys Cys Val Ile
141          325                      330                      335
143 cct atg gga gga cca ctt ccg cgg att cct caa aat gtt atg gct att      1056
144 Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile
145          340                      345                      350
147 ggt ggg aat tca ggg ata gtt cat cca tca aca ggg tac atg gtg gct      1104
148 Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala
149          355                      360                      365
151 agg agc atg gct tta gca cca gta cta gct gaa gcc atc gtc gag ggg      1152
152 Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly
153          370                      375                      380
155 ctt ggc tca aca aga atg ata aga ggg tct caa ctt tac cat aga gtt      1200
156 Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val
157 385                      390                      395                      400
159 tgg aat ggt ttg tgg cct ttg gat aga aga tgt gtt aga gaa tgt tat      1248
160 Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr
161          405                      410                      415
163 tca ttt ggg atg gag aca ttg ttg aag ctt gat ttg aaa ggg act agg      1296
164 Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg
165          420                      425                      430
167 aga ttg ttt gac gct ttc ttt gat ctt gat cct aaa tac tgg caa ggg      1344
168 Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly
169          435                      440                      445
171 ttc ctt tct tca aga ttg tct gtc aaa gaa ctt ggt tta ctc agc ttg      1392
172 Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu
173          450                      455                      460
175 tgt ctt ttc gga cat ggc tca aac atg act agg ttg gat att gtt aca      1440
176 Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr
177 465                      470                      475                      480
179 aaa tgt cct ctt cct ttg gtt aga ctg att ggc aat cta gca ata gag      1488
180 Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu
181          485                      490                      495
183 agc ctt tgaatgtgaa aagtttgaat cattttcttc attttaattt ctttgattat      1544
184 Ser Leu
187 tttcatatatt tctcaattgc aaaagtgaga taagagctac atactgtcaa caaataaact      1604
189 actattggaa agttaaaata tgtgtttgtt gtatgttatt ctaatggaat ggattttgta      1664
191 aa      1666
194 <210> SEQ ID NO: 2
195 <211> LENGTH: 498
196 <212> TYPE: PRT

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197 <213> ORGANISM: Lycopersicon esculentum
200 <400> SEQUENCE: 2
202 Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Leu Ser Ser Pro
203 1 5 10 15
206 Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro
207 20 25 30
210 Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser
211 35 40 45
214 Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu
215 50 55 60
218 Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala
219 65 70 75 80
222 Gln Phe Asp Val Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu
223 85 90 95
226 Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro
227 100 105 110
230 Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu
231 115 120 125
234 Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met
235 130 135 140
238 Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro
239 145 150 155 160
242 Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser
243 165 170 175
246 Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val
247 180 185 190
250 Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys
251 195 200 205
254 Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe
255 210 215 220
258 Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly
259 225 230 235 240
262 Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val
263 245 250 255
266 Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg
267 260 265 270
270 Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp
271 275 280 285
274 Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val
275 290 295 300
278 Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His
279 305 310 315 320
282 Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Glu Lys Cys Val Ile
283 325 330 335
286 Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile
287 340 345 350
290 Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala
291 355 360 365
294 Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly

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295      370      375      380
298 Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val
299 385      390      395      400
302 Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr
303      405      410      415
306 Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg
307      420      425      430
310 Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly
311      435      440      445
314 Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu
315      450      455      460
318 Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr
319 465      470      475      480
322 Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu
323      485      490      495
326 Ser Leu
330 <210> SEQ ID NO: 3
331 <211> LENGTH: 1771
332 <212> TYPE: DNA
333 <213> ORGANISM: Haematococcus pluvialis
336 <220> FEATURE:
337 <221> NAME/KEY: CDS
338 <222> LOCATION: (166)..(1155)
342 <400> SEQUENCE: 3
343 ggcacgagct tgcacgcaag tcagcgcgcg caagtcaaca cctgccgggtc cacagcctca      60
345 aataataaag agctcaagcg tttgtgcgcc tcgacgtggc cagtctgcac tgccttgaac      120
347 ccgcgagagt cccgcgcgcac tgactgccat agcacagcta gacga atg cag cta gca      177
348                               Met Gln Leu Ala
349                               1
351 gcg aca gta atg ttg gag cag ctt acc gga agc gct gag gca ctc aag      225
352 Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys
353 5      10      15      20
355 gag aag gag aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg      273
356 Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp
357      25      30      35
359 gcg acc cag tac tcg ctt ccg tca gaa gag tca gac gcg gcc cgc ccg      321
360 Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro
361      40      45      50
363 gga ctg aag aat gcc tac aag cca cca cct tcc gac aca aag ggc atc      369
364 Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile
365      55      60      65
367 aca atg gcg cta cgt gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac      417
368 Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala Val Phe Leu His
369      70      75      80
371 gcc att ttt caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg      465
372 Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp
373 85      90      95      100
375 ctg ccc gtg tca gat gcc aca gct cag ctg gtt agc ggc acg agc agc      513
376 Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Thr Ser Ser

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/569,022

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L:18 M:270 C: Current Application Number differs, Replaced Current Application No

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date